

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) ADDRESSEE: E. I. DUPONT DE NEMOURS AND COMPANY
 - (B) STREET: 1007 MARKET STREET
 - (C) CITY: WILMINGTON
 - (D) STATE: DELAWARE
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 19898
 - (G) TELEPHONE: 302-992-4926
 - (H) TELEFAX: 302-773-0164
 - (I) TELEX: 6717325
- (ii) TITLE OF INVENTION: PLANT SUG1 HOMOLOGS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: MICROSOFT WINDOWS 95
 - (D) SOFTWARE: MICROSOFT WORD VERSION 7.0A
- (v) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/893,401
 - (B) FILING DATE: JULY 11, 1997
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: MAJARIAN, WILLIAM R.
 - (B) REGISTRATION NUMBER: 41,173
 - (C) REFERENCE/DOCKET NUMBER: BB-1095-A

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Soybean

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT CTT GTA GGA GTT GAA CTG AAG CAT GCG GCG GAG GGC GTA CCG	48
Met Ala Leu Val Gly Val Glu Leu Lys His Ala Ala Glu Gly Val Pro	
1 5 10 15	
GAG GCG AAT TGC TCC GCC AAG CCC ACC AAG CAG GGC GAG GGC CTC CGC	96
Glu Ala Asn Cys Ser Ala Lys Pro Thr Lys Gln Gly Glu Gly Leu Arg	
20 25 30	
CAC TAC TAT TCT CTC AAC ATC CAC GAG CAT CAG CTC CTT CTT CGC CAA	144
His Tyr Tyr Ser Leu Asn Ile His Glu His Gln Leu Leu Arg Gln	
35 40 45	
AAG ACT CAT AAC CTC AAC CGT CTC GAG GCT CAG AGA AAC GAC CTC AAT	192
Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg Asn Asp Leu Asn	
50 55 60	
TCT AGG GTG AGG ATG CTG CGC GAA GAA TTA CAG CTT CTG CAG GAA CCC	240
Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro	
65 70 75 80	
GGC TCT TAT GTC GGT GAA GTT GTC AAA GTA ATG GGC AAG AAC AAA GTC	288
Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly Lys Asn Lys Val	
85 90 95	
CTT GTC AAG GTC CAC CCA GAA GGA AAA TAT GTT GTT GAC ATT GAC AAA	336
Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys	
100 105 110	
AAT ATT GAC ATT ACA AAG ATT ACT CCA TCC ACT AGA GTT GCA CTC CGC	384
Asn Ile Asp Ile Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg	
115 120 125	
AAC GAC AGT TAT GTT CTT CAC TTA GTT CTG CCA AGT AAA GTT GAT CCA	432
Asn Asp Ser Tyr Val Leu His Leu Val Leu Pro Ser Lys Val Asp Pro	
130 135 140	
TTG GTC AAT CTG ATG AAA GTT GAG AAA GTT CCC GAT TCT ACA TAT GAC	480
Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp	
145 150 155 160	
ATG ATT GGT GGT TTA GAC CAG CAA ATT AAA GAA ATA AAA GAG GTC ATT	528
Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile	
165 170 175	
GAG CTA CCA ATC AAA CAT CCT GAG CTG TTT GAA AGT CTT GGA ATT GCA	576
Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala	
180 185 190	

CAA CCA AAG GGT GTC CTG CTC TAT GGG CCA CCT GGT ACA GGT AAA ACA Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr 195 200 205	624
TTG TTG GCT AGG GCA GTG GCT CAT CAT ACT GAC TGT ACA TTC ATC AGG Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg 210 215 220	672
GTG TCT GGT TCT GAG TTA GTT CAG AAA TAC ATT GGA GAA GGT TCT AGA Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg 225 230 235 240	720
ATG GTC AGG GAA CTT TTT GTT ATG GCC AGG GAA CAT GCT CCA TCA ATT Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile 245 250 255	768
ATC TTC ATG GAT GAA ATT GAC AGT ATT GGA TCT GCT CGG ATG GAA TCT Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser 260 265 270	816
GGA AGT GGC AAC GGT GAT AGT GAG GTA CAG CGT ACT ATG CTG GAA CTT Gly Ser Gly Asn Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu 275 280 285	864
CTC AAC CAG TTG GAT GGA TTT GAA GCT TCA AAT AAG ATC AAG GTT TTG Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val Leu 290 295 300	912
ATG GCC ACC AAT CGG ATT GAT ATC CTG GAT CAA GCC CTC CTT AGA CCA Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro 305 310 315 320	960
GGA CGG ATA GAC CGG AAA ATT GAA TTT CCA ACC CCT AAT GAA GAG TCT Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Thr Pro Asn Glu Glu Ser 325 330 335	1008
CGG CTG GAT ATT TTG AAA ATC CAT TCT AGA AGA ATG AAT TTA ATG CGT Arg Leu Asp Ile Leu Lys Ile His Ser Arg Arg Met Asn Leu Met Arg 340 345 350	1056
GGC ATT GAT TTG AAG AAG ATT GCC GAG AAG ATG AAT GGA GCA TCT GGT Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser Gly 355 360 365	1104
GCT GAA CTT AAG GCT GTT TGC ACT GAA GCT GGA ATG TTT GCT TTG AGG Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg 370 375 380	1152
GAG CGG AGG GTA CAC GTG ACT CAG GAG GAT TTT GAG ATG GCC GTG GCG Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala 385 390 395 400	1200
AAG GTG ATG AAA AAG GAG ACT GAA AAA AAC ATG TCA TTG CGG AAG TTG Lys Val Met Lys Lys Glu Thr Glu Lys Asn Met Ser Leu Arg Lys Leu 405 410 415	1248
TGG AAG Trp Lys	1254

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Val Gly Val Glu Leu Lys His Ala Ala Glu Gly Val Pro
 1 5 10 15
 Glu Ala Asn Cys Ser Ala Lys Pro Thr Lys Gln Gly Glu Gly Leu Arg
 20 25 30
 His Tyr Tyr Ser Leu Asn Ile His Glu His Gln Leu Leu Leu Arg Gln
 35 40 45
 Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg Asn Asp Leu Asn
 50 55 60
 Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro
 65 70 75 80
 Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly Lys Asn Lys Val
 85 90 95
 Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys
 100 105 110
 Asn Ile Asp Ile Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg
 115 120 125
 Asn Asp Ser Tyr Val Leu His Leu Val Leu Pro Ser Lys Val Asp Pro
 130 135 140
 Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp
 145 150 155 160
 Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile
 165 170 175
 Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala
 180 185 190
 Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr
 195 200 205
 Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg
 210 215 220
 Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg
 225 230 235 240
 Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile
 245 250 255
 Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser
 260 265 270
 Gly Ser Gly Asn Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu
 275 280 285
 Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val Leu
 290 295 300
 Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro
 305 310 315 320

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CTC	ATG	AAA	GTT	GAG	AAG	GTT	CCG	GAT	TCT	ACC	TAT	GAT	ATG	ATT	GGA	383
Leu	Met	Lys	Val	Glu	Lys	Val	Pro	Asp	Ser	Thr	Tyr	Asp	Met	Ile	Gly	
			115					120					125			
GGC	CTT	GAC	CAG	CAA	ATT	AAA	GAG	ATC	AAA	GAG	GTC	ATT	GAG	CTT	CCA	431
Gly	Leu	Asp	Gln	Gln	Ile	Lys	Glu	Ile	Lys	Glu	Val	Ile	Glu	Leu	Pro	
		130					135					140				
ATC	AAA	CAT	CCG	GAA	CTG	TTT	GAG	AGC	CTT	GGA	ATT	GCG	CAA	CCA	AAG	479
Ile	Lys	His	Pro	Glu	Leu	Phe	Glu	Ser	Leu	Gly	Ile	Ala	Gln	Pro	Lys	
	145					150					155					
GGT	GTC	CTT	CTT	TAT	GGA	CCT	CCG	GGC	ACA	GGA	AAG	ACA	TTG	TTG	GCA	527
Gly	Val	Leu	Leu	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Leu	Ala	
160					165					170					175	
CGT	GCG	GTT	GCT	CAT	CAC	ACT	GAC	TGC	ACC	TTC	ATC	AGG	GTG	TCT	GGT	575
Arg	Ala	Val	Ala	His	His	Thr	Asp	Cys	Thr	Phe	Ile	Arg	Val	Ser	Gly	
			180					185						190		
TCT	GAG	TTG	GTT	CAG	AAG	TAT	ATT	GGT	GAG	GGC	TCC	CGG	ATG	GTT	AGG	623
Ser	Glu	Leu	Val	Gln	Lys	Tyr	Ile	Gly	Glu	Gly	Ser	Arg	Met	Val	Arg	
			195					200					205			
GAA	CTC	TTT	GTT	ATG	GCC	AGG	GAA	CAT	GCA	CCA	TCC	ATT	ATA	TTT	ATG	671
Glu	Leu	Phe	Val	Met	Ala	Arg	Glu	His	Ala	Pro	Ser	Ile	Ile	Phe	Met	
		210					215					220				
GAT	GAA	ATT	GAC	TCT	ATC	GGA	TCT	GCT	AGA	ATG	GAG	TCT	GGA	ACT	GGC	719
Asp	Glu	Ile	Asp	Ser	Ile	Gly	Ser	Ala	Arg	Met	Glu	Ser	Gly	Thr	Gly	
	225					230					235					
AAC	GGT	GAC	AGT	GAA	GTT	CAG	CGT	ACT	ATG	CTT	GAA	CTT	CTA	AAC	CAG	767
Asn	Gly	Asp	Ser	Glu	Val	Gln	Arg	Thr	Met	Leu	Glu	Leu	Leu	Asn	Gln	
240					245					250					255	
CTC	GAT	GGT	TTT	GAA	GCA	TCA	AAC	AAA	ATT	AAG	GTT	TTG	ATG	GCA	ACG	815
Leu	Asp	Gly	Phe	Glu	Ala	Ser	Asn	Lys	Ile	Lys	Val	Leu	Met	Ala	Thr	
				260				265						270		
AAC	AGA	ATA	GAC	ATT	TTG	GAT	CAA	GCC	CTT	CTG	AGG	CCT	GGC	CGC	ATA	863
Asn	Arg	Ile	Asp	Ile	Leu	Asp	Gln	Ala	Leu	Leu	Arg	Pro	Gly	Arg	Ile	
			275				280						285			
GAC	AGG	AAG	ATT	GAA	TTT	CCA	AAT	CCT	AAC	GAG	GAT	TCA	CGT	TTC	GAT	911
Asp	Arg	Lys	Ile	Glu	Phe	Pro	Asn	Pro	Asn	Glu	Asp	Ser	Arg	Phe	Asp	
		290					295					300				
ATC	TTG	AAG	ATC	CAT	TCA	AGA	AAA	ATG	AAC	TTG	ATG	CGT	GGC	ATT	GAT	959
Ile	Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met	Arg	Gly	Ile	Asp	
	305					310					315					
CTG	AAA	AAG	ATC	GCG	GAA	AAG	ATG	AAT	GGG	GCC	TCA	GGA	GCT	GAG	CTC	1007
Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser	Gly	Ala	Glu	Leu	
320					325					330					335	
AAG	GCC	GTC	TGC	ACA	GAG	GCT	GGA	ATG	TTT	GCT	CTT	CGT	GAG	AGA	AGG	1055
Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu	Arg	Glu	Arg	Arg	
				340				345					350			
GTG	CAC	GTT	ACC	CAG	GAG	GAC	TTC	GAG	ATG	GCA	GTG	GCC	AAG	GTG	ATG	1103
Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val	Ala	Lys	Val	Met	
			355				360						365			

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AAG AAA GAC ACG GAG AAG AAC ATG TCC CTG CGC AAG CTC TGG AAG
 Lys Lys Asp Thr Glu Lys Asn Met Ser Leu Arg Lys Leu Trp Lys
 370 375 380

1148

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu His Ile His Asp Leu Gln Leu Gln Ile Arg Gln Lys Thr His Asn
 1 5 10 15
 Leu Asn Arg Leu Glu Ala Gln Arg Asn Asp Leu Asn Ser Arg Val Arg
 20 25 30
 Met Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu Pro Gly Ser Tyr Val
 35 40 45
 Gly Glu Val Val Lys Val Met Gly Lys Ser Lys Val Leu Val Lys Val
 50 55 60
 His Pro Glu Gly Lys Tyr Val Val Asp Ile Asp Lys Ser Ile Asp Ile
 65 70 75 80
 Thr Lys Ile Thr Pro Ser Thr Arg Val Ala Leu Arg Asn Asp Ser Tyr
 85 90 95
 Met Leu His Leu Ile Leu Pro Ser Lys Val Asp Pro Leu Val Asn Leu
 100 105 110
 Met Lys Val Glu Lys Val Pro Asp Ser Thr Tyr Asp Met Ile Gly Gly
 115 120 125
 Leu Asp Gln Gln Ile Lys Glu Ile Lys Glu Val Ile Glu Leu Pro Ile
 130 135 140
 Lys His Pro Glu Leu Phe Glu Ser Leu Gly Ile Ala Gln Pro Lys Gly
 145 150 155 160
 Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Arg
 165 170 175
 Ala Val Ala His His Thr Asp Cys Thr Phe Ile Arg Val Ser Gly Ser
 180 185 190
 Glu Leu Val Gln Lys Tyr Ile Gly Glu Gly Ser Arg Met Val Arg Glu
 195 200 205
 Leu Phe Val Met Ala Arg Glu His Ala Pro Ser Ile Ile Phe Met Asp
 210 215 220
 Glu Ile Asp Ser Ile Gly Ser Ala Arg Met Glu Ser Gly Thr Gly Asn
 225 230 235 240
 Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu Leu Asn Gln Leu
 245 250 255
 Asp Gly Phe Glu Ala Ser Asn Lys Ile Lys Val Leu Met Ala Thr Asn
 260 265 270

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Arg Ile Asp Ile Leu Asp Gln Ala Leu Leu Arg Pro Gly Arg Ile Asp
 275 280 285

Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Asp Ser Arg Phe Asp Ile
 290 295 300

Leu Lys Ile His Ser Arg Lys Met Asn Leu Met Arg Gly Ile Asp Leu
 305 310 315 320

Lys Lys Ile Ala Glu Lys Met Asn Gly Ala Ser Gly Ala Glu Leu Lys
 325 330 335

Ala Val Cys Thr Glu Ala Gly Met Phe Ala Leu Arg Glu Arg Arg Val
 340 345 350

His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala Lys Val Met Lys
 355 360 365

Lys Asp Thr Glu Lys Asn Met Ser Leu Arg Lys Leu Trp Lys
 370 375 380

2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCAAGCCAA CAAGCAAGAC CGCTTCTGCT TGTGATCCGA AACCTTTCTT CGAACGCAAA	60
AAGAACCCCA CCCGACGTAC CGCGAGCCGG CGATGGCGAC GGTGGCGATG GACATCTCGA	120
AGCCCACGCC GGCAGCGTCC GGTGACGAGG CAGCAGCGGC GCGGAAGGGG AGGAGCGGCG	180
GCGGGGGCGA GGGGCTGCGG CAGTACTACC TGCAGCACAT CCATGACCTG CAGCTCCAGA	240
TCCGGCAGAA GACCCATAAC CTCAACCGCC TCGAGGCCCA GCGCAACGAC CTCAACTCCC	300
GAGTTAGAAT GCTCAGGGAA GAGTTGCAGT TGCTTCAAGA GCCTGGCTCA TATGTTGGTG	360
AGGTGGTGAA GGTCATGGGG AAATCAAAGG TTCTGGTGAA GGTACATCCC GAAGGCAAAT	420
ATGTGGTGGA TATAGATAAG AGCATTGATA TCACTAAGAT CACACCTTCA ACAAGAGTTG	480
CTCTTCGGAA TGACAGCTAT ATGCTCCATC TGATCCTACC AAGCAAAGTT GATCCATTGG	540
TCAATCTCAT GAAAGTTGAG AAGGTTCCGG ATTCTACCTA TGATATGATT GGAGGCCTTG	600
ACCAGCAAAT TAAAGAGATC AAAGAGGTCA TTGAGCTTCC AATCAAACAT CCGGAACTGT	660
TTGAGAGCCT TGAATTGCG CAACCAAAGG GTGTCCTTCT TTATGGACCT CCGGGCACAG	720
GAAAGACATT GTTGGCACGT GCGGTTGCTC ATCACACTGA CTGCACCTTC ATCAGGGTGT	780
CTGGTTCTGA GTTGGTTCAG AAGTATATTG GTGAGGGCTC CCGGATGGTT AGGGAAGTCT	840
TTGTTATGGC CAGGGAACAT GCACCATCCA TTATATTTAT GGATGAAATT GACTCTATCG	900
GATCTGCTAG AATGGAGTCT GGAAGTGGCA ACGGTGACAG TGAAGTTCAG CGTACTATGC	960
TTGAAGTTCT AAACCAGCTC GATGGTTTTG AAGCATCAAA CAAAATTAAG GTTTTGATGG	1020

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CAACGAACAG AATAGACATT TTGGATCAAG CCCTTCTGAG GCCTGGCCGC ATAGACAGGA 1080
 AGATTGAATT TCCAAATCCT AACGAGGATT CACGTTTCGA TATCTTGAAG ATCCATTCAA 1140
 GAAAAATGAA CTTGATGCGT GGCATTGATC TGAAAAAGAT CGCGGAAAAG ATGAATGGGG 1200
 CCTCAGGAGC TGAGCTCAAG GCCGTCTGCA CAGAGGCTGG AATGTTTGCT CTTCGTGAGA 1260
 GAAGGGTGCA CGTTACCCAG GAGGACTTCG AGATGGCAGT GGCCAAGGTG ATGAAGAAAG 1320
 ACACGGAGAA GAACATGTCC CTGCGCAAGC TCTGGAAG 1358

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Thr Val Ala Met Asp Ile Ser Lys Pro Thr Pro Ala Ala Ser
 1 5 10 15
 Gly Asp Glu Ala Ala Ala Ala Lys Gly Arg Ser Gly Gly Gly Gly
 20 25 30
 Glu Gly Leu Arg Gln Tyr Tyr Leu Gln His Ile His Asp Leu Gln Leu
 35 40 45
 Gln Ile Arg Gln Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg
 50 55 60
 Asn Asp Leu Asn Ser Arg Val Arg Met Leu Arg Glu Glu Leu Gln Leu
 65 70 75 80
 Leu Gln Glu Pro Gly Ser Tyr Val Gly Glu Val Val Lys Val Met Gly
 85 90 95
 Lys Ser Lys Val Leu Val Lys Val His Pro Glu Gly Lys Tyr Val Val
 100 105 110
 Asp Ile Asp Lys Ser Ile Asp Ile Thr Lys Ile Thr Pro Ser Thr Arg
 115 120 125
 Val Ala Leu Arg Asn Asp Ser Tyr Met Leu His Leu Ile Leu Pro Ser
 130 135 140
 Lys Val Asp Pro Leu Val Asn Leu Met Lys Val Glu Lys Val Pro Asp
 145 150 155 160
 Ser Thr Tyr Asp Met Ile Gly Gly Leu Asp Gln Gln Ile Lys Glu Ile
 165 170 175
 Lys Glu Val Ile Glu Leu Pro Ile Lys His Pro Glu Leu Phe Glu Ser
 180 185 190
 Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly
 195 200 205
 Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys
 210 215 220

Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Tyr Ile Gly
 225 230 235 240
 Glu Gly Ser Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His
 245 250 255
 Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ala
 260 265 270
 Arg Met Glu Ser Gly Thr Gly Asn Gly Asp Ser Glu Val Gln Arg Thr
 275 280 285
 Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Ser Asn Lys
 290 295 300
 Ile Lys Val Leu Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Gln Ala
 305 310 315 320
 Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro
 325 330 335
 Asn Glu Asp Ser Arg Phe Asp Ile Leu Lys Ile His Ser Arg Lys Met
 340 345 350
 Asn Leu Met Arg Gly Ile Asp Leu Lys Lys Ile Ala Glu Lys Met Asn
 355 360 365
 Gly Ala Ser Gly Ala Glu Leu Lys Ala Val Cys Thr Glu Ala Gly Met
 370 375 380
 Phe Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu
 385 390 395 400
 Met Ala Val Ala Lys Val Met Lys Lys Asp Thr Glu Lys Asn Met Ser
 405 410 415
 Leu Arg Lys Leu Trp Lys
 420

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Leu Asp Gly Pro Glu Gln Met Glu Leu Glu Glu Gly Lys Ala
 1 5 10 15
 Gly Ser Gly Leu Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln
 20 25 30
 Leu Ile Val Asn Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln
 35 40 45
 Arg Asn Glu Leu Asn Ala Lys Val Arg Leu Leu Arg Glu Glu Leu Gln
 50 55 60

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Leu Leu Gln Glu Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met
 65 70 75 80
 Asp Lys Lys Lys Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val
 85 90 95
 Val Asp Val Asp Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys
 100 105 110
 Arg Val Ala Leu Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro
 115 120 125
 Asn Lys Val Asp Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro
 130 135 140
 Asp Ser Thr Tyr Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu
 145 150 155 160
 Ile Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu
 165 170 175
 Ala Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro
 180 185 190
 Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp
 195 200 205
 Cys Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile
 210 215 220
 Gly Glu Gly Ala Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu
 225 230 235 240
 His Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser
 245 250 255
 Ser Arg Leu Glu Gly Gly Ser Gly Gly Asp Ser Glu Val Gln Arg Thr
 260 265 270
 Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn
 275 280 285
 Ile Lys Val Ile Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Ser Ala
 290 295 300
 Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro
 305 310 315 320
 Asn Glu Glu Ala Arg Leu Asp Ile Leu Lys Ile His Ser Arg Lys Met
 325 330 335
 Asn Leu Thr Arg Gly Ile Asn Leu Arg Lys Ile Ala Glu Leu Met Pro
 340 345 350
 Gly Ala Ser Gly Ala Glu Val Lys Gly Val Cys Thr Glu Ala Gly Met
 355 360 365
 Tyr Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu
 370 375 380
 Met Ala Val Ala Lys Val Met Gln Lys Asp Ser Glu Lys Asn Met Ser
 385 390 395 400
 Ile Lys Lys Leu Trp Lys
 405

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Yeast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Thr Ala Ala Val Thr Ser Ser Asn Ile Val Leu Glu Thr His Glu
  1          5          10
Ser Gly Ile Lys Pro Tyr Phe Glu Gln Lys Ile Gln Glu Thr Glu Leu
  20          25          30
Lys Ile Arg Ser Lys Thr Glu Asn Val Arg Arg Leu Glu Ala Gln Arg
  35          40          45
Asn Ala Leu Asn Asp Lys Val Arg Phe Ile Lys Asp Glu Leu Arg Leu
  50          55          60
Leu Gln Glu Pro Gly Ser Tyr Val Gly Glu Val Ile Lys Ile Val Ser
  65          70          75
Asp Lys Lys Val Leu Val Lys Val Gln Pro Glu Gly Lys Tyr Ile Val
  85          90          95
Asp Val Ala Lys Asp Ile Asn Val Lys Asp Leu Lys Ala Ser Gln Arg
 100          105          110
Val Cys Leu Arg Ser Asp Ser Tyr Met Leu His Lys Val Leu Glu Asn
 115          120          125
Lys Ala Asp Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro Asp
 130          135          140
Ser Thr Tyr Asp Met Val Gly Gly Leu Thr Lys Gln Ile Lys Glu Ile
 145          150          155
Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu Ser
 165          170          175
Leu Gly Ile Ala Gln Pro Lys Gly Val Ile Leu Tyr Gly Pro Pro Gly
 180          185          190
Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys
 195          200          205
Lys Phe Ile Arg Val Ser Gly Ala Glu Leu Val Gln Lys Tyr Ile Gly
 210          215          220
Glu Gly Ser Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His
 225          230          235
Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Thr
 245          250          255
Arg Val Glu Gly Ser Gly Gly Gly Asp Ser Glu Val Gln Arg Thr Met
 260          265          270

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Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Thr Ser Lys Asn Ile
 275 280 285
 Lys Ile Ile Met Ala Thr Asn Arg Leu Asp Ile Leu Asp Pro Ala Leu
 290 295 300
 Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro Ser
 305 310 315 320
 Val Ala Ala Arg Ala Glu Ile Leu Arg Ile His Ser Arg Lys Met Asn
 325 330 335
 Leu Thr Arg Gly Ile Asn Leu Arg Lys Val Ala Glu Lys Met Asn Gly
 340 345 350
 Cys Ser Gly Ala Asp Val Lys Gly Val Cys Thr Glu Ala Gly Met Tyr
 355 360 365
 Ala Leu Arg Glu Arg Arg Ile His Val Thr Gln Glu Asp Phe Glu Leu
 370 375 380
 Ala Val Gly Lys Val Met Asn Lys Asn Gln Glu Thr Ala Ile Ser Val
 385 390 395 400
 Ala Lys Leu Phe Lys
 405

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Human Tripl

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Leu Asp Gly Pro Glu Gln Met Glu Leu Glu Glu Gly Lys Ala
 1 5 10 15
 Gly Ser Gly Leu Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln
 20 25 30
 Leu Ile Val Asn Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln
 35 40 45
 Arg Asn Glu Leu Asn Ala Lys Val Arg Leu Leu Arg Glu Glu Leu Gln
 50 55 60
 Leu Leu Gln Glu Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met
 65 70 75 80
 Asp Lys Lys Lys Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val
 85 90 95
 Val Asp Val Asp Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys
 100 105 110
 Arg Val Ala Leu Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro
 115 120 125

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Asn Lys Val Asp Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro
 130 135 140
 Asp Ser Thr Tyr Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu
 145 150 155 160
 Ile Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu
 165 170 175
 Ala Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro
 180 185 190
 Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp
 195 200 205
 Cys Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile
 210 215 220
 Gly Glu Gly Ala Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu
 225 230 235 240
 His Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser
 245 250 255
 Ser Arg Leu Glu Gly Gly Ser Gly Gly Ser Ser Glu Val Gln Arg Gln
 260 265 270
 Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn
 275 280 285
 Ile Lys Val Ile Met Ala Thr Asn Arg Ile Asp Met Leu Asp Ser Ala
 290 295 300
 Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro
 305 310 315 320
 Asn Glu Glu Ala Arg Leu Asp Ile Leu Lys Ile His Ser Arg Lys Met
 325 330 335
 Asn Leu Thr Arg Gly Ile Asn Leu Arg Lys Ile Ala Glu Leu Met Pro
 340 345 350
 Gly Ala Ser Gly Ala Glu Val Lys Gly Val Cys Thr Glu Ala Gly Met
 355 360 365
 Tyr Ala Leu Arg Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu
 370 375 380
 Met Ala Val Ala Lys Val Met Gln Lys Asp Ser Glu Lys Asn Met Ser
 385 390 395 400
 Ile Lys Lys Leu Trp Lys
 405

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 406 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

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(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Human p45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Met Ala Leu Asp Gly Pro Glu Gln Met Glu Leu Glu Glu Gly Lys Ala
1          5          10          15
Gly Ser Gly Leu Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln
20          25          30
Leu Ile Val Asn Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln
35          40          45
Arg Asn Glu Leu Asn Ala Lys Val Arg Leu Leu Arg Arg Glu Leu Gln
50          55          60
Leu Leu Gln Glu Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met
65          70          75          80
Asp Lys Lys Lys Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val
85          90          95
Val Asp Val Asp Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys
100         105         110
Arg Val Ala Leu Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro
115         120         125
Asn Lys Val Asp Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro
130         135         140
Asp Ser Thr Tyr Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu
145         150         155         160
Ile Lys Glu Val Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu
165         170         175
Ala Leu Gly Ile Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro
180         185         190
Gly Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp
195         200         205
Cys Thr Phe Ile Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile
210         215         220
Gly Glu Gly Ala Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu
225         230         235         240
His Ala Pro Ser Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser
245         250         255
Ser Arg Leu Glu Gly Gly Ser Gly Gly Asp Ser Glu Val Gln Arg Thr
260         265         270
Met Leu Glu Leu Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn
275         280         285
Ile Lys Val Ile Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Ser Ala
290         295         300
Leu Leu Arg Pro Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro
305         310         315         320

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Thr Val Ala Met Asp Ile Ser Lys Pro Thr Pro Val Ala Ser
 1 5 10 15
 Gly Asp Glu Ala Ala Ala Ala Lys Gly Arg Ser Gly Gly Gly Gly
 20 25 30
 Glu Gly Leu Arg Gln Tyr Tyr Leu Gln His Ile His Asp Leu Gln Leu
 35 40 45
 Gln Ile Arg His Lys Thr His Asn Leu Asn Arg Leu Glu Ala Gln Arg
 50 55 60
 Asn Asp Leu Asn Ser Arg Val Arg Met Leu Arg Glu Asp Xaa Xaa Leu
 65 70 75 80
 Leu Xaa Glu Pro Gly Ser Tyr Val Gly Xaa Val Val Lys Ala Trp Gly
 85 90 95
 Asn Gln Arg Phe Trp Val Lys Val Asn Pro Glu Gly Lys Xaa Xaa Val
 100 105 110
 Asp Ile Asn
 115

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 593 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 (B) CLONE: rlr6.pk0064.e10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTTTAAACGG TACAGGAAAA ACGCTACTAG CTCGGGCAGT TGCTCATCAC ACCGACTGTA 60
 CCTTTATTAA GGGTGT CAGG TTCCGAGTTG GTTCAGAACT ATATTGGAGA GGGTTCCAGA 120
 ATGGTTCGTG AACTATTTGT GATGGCCANA GAGCATGCAC CATCCATAAT CTTTATGGAT 180
 GAAATAGACT CCATTGGATC TGCTANAATG CAGTCANGAT CTGGGGGTGG TGATAGTGAG 240
 GTTCAACGCA CTATGCTTGA TCTTCTGAAT CAACTTGATG GCTTTGAAGC ATCAAACANA 300
 ATTAAGGTCT TATGGCGACA AATANGATGG ATATTTTGA TCAAGCTCTC TGANGCCTGG 360
 TCGCATTGAT AGGAAGATGA ATTTCCAATC CGAATGAAGA TCCGCTTGAT ANTTGAAGAT 420
 CATTCAAGAA AAATGACTGA TCTGGATTGT CTGAAAAGAT GCAGAGAAAT GATGGGCNCT 480
 GGACAAACTA AGNGTCTNAC GAACAAGATT TGCCTCCAAA NAGGTATTCA CAGAGATCTA 540
 TGGGTGCAAG GTGAAAGNAC GAAGAATCCG NCACCGAATA AGANNCACCA ACC 593

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 amino acids
 (B) TYPE: amino acid

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(C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: rlr6.pk0064.e10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly	Thr	Gly	Lys	Thr	Leu	Leu	Ala	Arg	Ala	Val	Ala	His	His	Thr	Asp
1				5					10					15	
Cys	Thr	Phe	Xaa	Arg	Val	Ser	Gly	Ser	Glu	Leu	Val	Gln	Lys	Tyr	Ile
			20					25					30		
Gly	Glu	Gly	Ser	Arg	Met	Val	Arg	Glu	Leu	Phe	Val	Met	Ala	Xaa	Glu
		35					40					45			
His	Ala	Pro	Ser	Ile	Ile	Phe	Met	Asp	Glu	Ile	Asp	Ser	Ile	Gly	Ser
	50					55					60				
Ala	Xaa	Met	Gln	Ser	Xaa	Ser	Gly	Gly	Gly	Asp	Ser	Glu	Val	Gln	Arg
65					70				75						80
Thr	Met	Leu	Asp	Leu	Leu	Asn	Gln	Leu	Asp	Gly	Phe	Glu	Ala	Ser	Asn
				85					90					95	
Xaa	Ile	Lys	Val	Xaa	Met	Ala	Thr	Asn	Xaa	Met	Asp	Ile	Leu	Asp	Gln
			100					105					110		
Ala	Leu	Xaa	Xaa	Pro	Gly	Arg	Ile	Asp	Arg	Lys	Met	Asn	Phe		
	115						120					125			